

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Mc Wherter, Charles
Feng, Yiqing
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Streeter, Philip
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Minster, Nancy
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(ii) TITLE OF THE INVENTION: Circular Permuteins of FLT3 Ligand

(iii) NUMBER OF SEQUENCES: 151

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 77002

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: CD
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unknown
(B) FILING DATE: 20-AUG-2003
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/955,090
(B) FILING DATE: 21-OCT-97

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/030,094
(B) FILING DATE: 25-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5				10						15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Ala	Leu
			35				40				45				
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
			50				55			60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65				70				75				80			
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
			85					90				95			
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100				105				110				
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
			115				120				125				
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
			130			135									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1					5				10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25				30			
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
			35				40				45				
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
			50				55			60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65				70				75				80			
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
			85					90				95			

Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
100								105				110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
115							120				125				
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
130						135				140					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1								10						15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
								20		25			30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
								35		40		45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
								50		55		60			
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
								65		70		75		80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val
								85		90			95		
Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu
								100		105			110		
Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu						
								115		120					

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1								5			10			15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
								20		25		30			
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
								35		40		45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
								50		55		60			
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile

65	70	75	80												
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85				90					95		
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
				100				105				110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
				115				120			125				
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
				130				135							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1								10					15		
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
								20	25				30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
								35	40			45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
								50	55			60			
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
								65	70			75		80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
								85	90			95			
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
								100	105			110			
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
								115	120			125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
								130	135			140			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1								10					15		
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
								20	25			30			

Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu
 35 40 45
 Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val
 50 55 60
 Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
 65 70 75 80
 His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg
 85 90 95
 Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln
 100 105 110
 Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys
 115 120 125
 Leu Glu Leu Gln Cys Gln Pro
 130 135

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
 1 5 10 15
 Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro
 20 25 30
 Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu
 35 40 45
 Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val
 50 55 60
 Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
 65 70 75 80
 His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg
 85 90 95
 Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln
 100 105 110
 Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys
 115 120 125
 Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1 5 10 15
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 20 25 30
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 35 40 45
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50 55 60
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 65 70 75 80
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 85 90 95
 Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser
 100 105 110
 Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
 115 120 125
 Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
 130 135 140
 Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
 145 150 155

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1 5 10 15
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 20 25 30
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 35 40 45
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50 55 60
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 65 70 75 80
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 85 90 95
 Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr
 100 105 110
 Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
 115 120 125
 Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr
 130 135 140
 Val Ala Ser Asn Leu Gln
 145 150

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1 5 10 15
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 20 25 30
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 35 40 45
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 50 55 60
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 65 70 75 80
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 85 90 95
 Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe
 100 105 110
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 115 120 125
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 130 135 140
 Gln
 145

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
 1 5 10 15
 Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
 20 25 30
 Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
 35 40 45
 Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
 50 55 60
 Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly
 65 70 75 80
 Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe
 85 90 95
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 100 105 110

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
115 120 125
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
130 135 140
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
1 5 10 15
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
20 25 30
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
35 40 45
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
50 55 60
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly
65 70 75 80
Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile
85 90 95
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu
100 105 110
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
115 120 125
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
130 135 140
Leu Lys Thr Val Ala Gly
145 150

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
1 5 10 15
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
20 25 30
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu

35	40	45													
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
50							55				60				
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly
65							70			75				80	
Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala
										85		90		95	
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val
								100		105			110		
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp
								115		120			125		
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala
								130		135			140		
Gly															
145															

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu
1								5		10				15	
Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr
								20		25				30	
Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser
								35		40			45		
Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly
								50		55			60		
Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
								65		70			75		80
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
								85		90			95		
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly
								100		105			110		
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr
								115		120			125		
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu
								130		135			140		
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro					
								145		150			155		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
1 5 10 15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
20 25 30
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
35 40 45
Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr Gln Asp
50 55 60
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile
65 70 75 80
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala
85 90 95
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val
100 105 110
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys
115 120 125
Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr
130 135 140
Lys Cys Ala Phe Gln Pro
145 150

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
1 5 10 15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
20 25 30
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
35 40 45
Ser Thr Leu Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His
50 55 60
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp
65 70 75 80
Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp
85 90 95
Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp
100 105 110
Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu
115 120 125
Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln
130 135 140
Pro
145

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
					20			25						30	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
					35			40					45		
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
					50			55			60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
					65			70			75			80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
					85			90				95			
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Ser		
					100			105			110				
Gly	Gly	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
					115			120			125				
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
					130			135			140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
					145			150			155				

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
					20			25						30	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
					35			40				45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
					50			55			60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
					65			70			75			80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro

	85		90		95										
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Thr		
				100		105					110				
Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val
				115		120					125				
Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr
				130		135					140				
Val	Ala	Ser	Asn	Leu	Gln										
				145		150									

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	
1									10					15		
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	
									20		25			30		
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	
									35		40			45		
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	
									50		55			60		
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	
									65		70			75		80
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	
									85		90			95		
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	
									100		105			110		
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	
									115		120			125		
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	
									130		135			140		
Ser																
145																

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly	Ser	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
1									5		10			15	

Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
20								25						30	
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys
35								40				45			
Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu
50								55				60			
Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn
65								70			75		80		
Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser
	85							90				95			
Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr
	100							105				110			
Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe
	115							120				125			
Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	
	130							135				140			

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
1								10						15	
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
								20			25			30	
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly
								35			40		45		
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr
								50			55		60		
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu
								65			70		75		80
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu
								85			90		95		
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu
								100			105		110		
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg
								115			120		125		
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly
								130			135		140		
Ser	Gly	Gly	Gly	Ser											
	145														

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Ser Gly Gly Ser Gly Gly Ser Gly Thr Gln Asp Cys Ser
1 5 10 15
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
20 25 30
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
35 40 45
Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala
50 55 60
Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln
65 70 75 80
Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys
85 90 95
Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile
100 105 110
Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro
115 120 125
Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln
130 135 140
Pro Asp Ser Ser Thr Leu
145 150

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Asp Glu Glu Leu Cys Gly Leu Trp Arg Leu Val Leu Ala Gln
1 5 10 15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
20 25 30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
35 40 45
Phe Gln Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
50 55 60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65 70 75 80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
85 90 95

Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser
100 105 110
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
115 120 125
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
130 135 140
Leu Gln
145

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
1 5 10 15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
20 25 30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
35 40 45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
50 55 60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65 70 75 80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
85 90 95
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Thr Gln Asp Cys
100 105 110
Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg
115 120 125
Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser
130 135 140
Asn Leu Gln
145

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
1 5 10 15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly

20	25	30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala		
35	40	45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser		
50	55	60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp		
65	70	75
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro		
85	90	95
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Thr		
100	105	110
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val		
115	120	125
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr		
130	135	140
Val Ala Ser Asn Leu Gln		
145	150	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln		
1	5	10
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly		
20	25	30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala		
35	40	45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser		
50	55	60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp		
65	70	75
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro		
85	90	95
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Gly		
100	105	110
Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp		
115	120	125
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr		
130	135	140
Pro Val Thr Val Ala Ser Asn Leu Gln		
145	150	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
1 5 10 15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
20 25 30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
35 40 45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
50 55 60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65 70 75 80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
85 90 95
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Gly
100 105 110
Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
115 120 125
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
130 135 140
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
145 150 155

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
      1           5           10           15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
      20          25          30
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
      35          40          45
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
      50          55          60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
      65          70          75          80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
      85          90          95
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Gly
      100         105         110
Ser Gly Gly Ser Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe
      115         120         125
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
      130         135         140

```

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
145 150 155 160
Gln

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
1 5 10 15
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
20 25 30
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val
35 40 45
Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro
50 55 60
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu
65 70 75 80
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
85 90 95
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
100 105 110
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Thr
115 120 125
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
130 135 140
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
145 150 155

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg
1 5 10 15
Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly
20 25 30
Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe
35 40 45
Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe Val

50	55	60													
Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val
65						70		75		80					
Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu
						85		90		95					
Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly
						100		105		110					
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	
						115		120		125					
His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser
						130		135		140					
Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val					
						145		150		155					

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr
1						5		10		15					
Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys
						20		25		30					
Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser
						35		40		45					
Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser
						50		55		60					
Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly
65						70		75		80					
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Thr	Gln	Asp	
						85		90		95					
Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile
						100		105		110					
Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala
						115		120		125					
Ser	Asn	Leu	Gln	Asp	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	
						130		135		140					
Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr					
						145		150		155					

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
1 5 10 15
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
20 25 30
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
35 40 45
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
50 55 60
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Ser Gly
65 70 75 80
Gly Gly Ser Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe
85 90 95
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
100 105 110
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
115 120 125
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
130 135 140
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
1 5 10 15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
20 25 30
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
35 40 45
Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
50 55 60
Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
65 70 75 80
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
85 90 95
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
100 105 110
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
115 120 125
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
130 135 140
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
145 150 155

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser
1							5			10				15	
Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser
							20			25				30	
Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly
							35			40			45		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Thr	Gln	Asp	
							50			55			60		
Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile
							65			70			75		80
Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala
							85			90			95		
Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val
							100			105			110		
Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys
							115			120			125		
Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr
							130			135			140		
Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu					
							145			150			155		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val
1							5			10			15		
Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu
							20			25			30		
Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Ser	Gly	Gly	
							35			40			45		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	
							50			55			60		
His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser
							65			70			75		80
Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln
							85			90			95		
Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg

100	105	110
Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu		
115	120	125
Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe		
130	135	140
Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln		
145	150	155

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Ser
1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Gly Ser Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Phe Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Phe Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Phe Gly Gly Asn Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Ser Asp Met Ala Gly
1 .5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Gly Gly Asn Gly
1 5

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Gly Gly Ser Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Gly Gly Ser Gly Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10 15
Gly Gly Gly Ser Gly
20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGACCATGG CNACCCAGGA CTGCTCCTTC CAA

33

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACTGAAGCTT AGGGCTGACA CTGCAGCTCC AG

32

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTGAAGCTT ACAGGGTTGA GGAGTCGGGC TG

32

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC

46

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC

46

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGTCCAAACT CATCAATGTA TC

22

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATGGCCATG GCCGACGAGG AGCTCTGCGG GGGCCTCT

38

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTAGAAGCT TACTGCAGGT TGGAGGCCAC GGTGAC

36

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CATGGCCATG GCCTCCAAGA TGCAAGGCTT GCTGGAGC

38

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTAGAAGCT TACCCAGCGA CAGTCTTGAG CCGCTC

36

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CATGGCCATG GCCCCCCCCC A GCTGTCTTCG CTTCGT

36

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTAGAAGCT TAGGGCTGAA AGGCACATT GGTGACA

37

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCCTGTCTGG CGGCAACGGC ACCCAGGACT GCTCCTTCCA AC

42

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCGGTAACGG CAGTGGAGGT AATGGCACCC AGGACTGCTC CTTCCAAC

48

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACGGCAGTGG TGGCAATGGG AGCGGCGGAA ATGGAACCCA GGACTGCTCC TTCCAAC

57

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTGCCGTTGC CGCCAGACAG GGTTGAGGAG TCGGGCTG

38

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTACCTCCA CTGCCGTTAC CGCCTGACAG GGTTGAGGAG TCGGGCTG

48

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCTCCCATTG CCACCACTGC CGTTACCTCC AGACAGGGTT GAGGAGTCGG GCTG

54

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GATGAGGATC CGGTGGCAAT GGGAGCGGGCG GAAATGGAAC CCAGGACTGC TCCTTCCACC

60

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GATGACGGAT CCGTTACCTC CAGACAGGGT TGAGGAGTCG GGCTG

45

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATGACGGAT CCGGAGGTAA TGGCACCCAG GACTGCTCCT TCCAAC

46

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAUTGCCATG GCCGACGAGG AGCTCTGCG

29

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAUTCAAGCT TACTGCAGGT TGGAGGCC

28

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAUTCGGGAT CCGGAGGTTC TGGCACCCAG GAUTGCTCC

39

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAUTGGGATC CGGTGGCAGT GGGAGCAGCG GATCTGGAAC C

41

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACTTGGGAT CCACTACCTC CAGACAGGGT TGAGGAGTC

39

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACTGACGGAT CCACCGCCA GGGTTGAGGA GTCGGGCTG

39

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACTGACGGAT CCACCTCCTG ACCCACCGCC CAGGGTTGAG GAGTCGGGCT G

51

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ACTGACGGAT CCACCTCCTG ACCCACCTCC TGACCCACCG CCCAGGGTTG AGGAGTCGGG
CTG

60

63

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACGTAAAGCT TACAGGGTTG AGGAGTCG

28

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCAGTGGAT CCGGAGGTAC CCAGGACTGC TCCTTCCAAC

40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCAGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AAC

43

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTCAGTGGAT CCGGAGGTGG CTCAGGGGA GGTAGTGGTA CCCAGGACTG CTCCTTCCAC

60

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTTGCCATGG CNTCNAAYCT GCARGAYGAR GARCTGTGCG GGGGCCTCTG GC GGCTG

57

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTTGCCATGG CNAAYCTGCA RGAYGARGAR CTGTGYGGGG GCCTCTGGCG GCTGGTC

57

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GTTGCCATGG CNCTGCARGA YGARGARCTG TGYYGGYGGCC TCTGGCGGCT GGTCCCTG

57

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GTTGCCATGG CNCARGAYGA RGARCTGTGY GGYGGYCTCT GGCGGCTGGT CCTGGCA

57

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTTGCCATGG CNGAYGARGA RCTGTGYGGY GGYCTCTGGC GGCTGGTCCT GGCACAG

57

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTGCCATGG CNGARGARCT GTGYGGYGGY CTCTGGCGGC TGGTCCTGGC ACAGCGC

57

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGCCATGG CNGARCTGTG YGGYGGYCTG TGGCGYCTGG TCCTGGCACA GCGCTGG

57

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTGCCATGG CNCTGTGYGG YGGYCTGTGG CGYCTGGTCC TGGCACAGCG CTGGATG

57

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAAGCT TAGGCCACGG TGACTGGGTA

30

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TATGCAAGCT TAGGAGGCCA CGGTGACTGG

30

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGCAAGCT TAGTTGGAGG CCACGGTGAC

30

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TATGCAAGCT TACAGGTTGG AGGCCACGGT

30

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGCAAGCT TACTGCAGGT TGGAGGCCAC

30

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TATGCAAGCT TAGTCCTGCA GGTTGGAGGC

30

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TATGCAAGCT TACTCGTCCT GCAGGTTGGA

30

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TATGCAAGCT TACTCCTCGT CCTGCAGGTT

30

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGC	GCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360

ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTTCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	300
TGGATCACTC	GCCAGAACTT	CTCCCCGGTGC	CTGGAGCTGC	AGTGTAGGCC	CGACTCCTCA	360
ACCCCTG						366

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGAACTCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGTACCCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360

ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCACTCAGG ACTGTTCTTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAATC	60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG	120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG	180
CTCAAGACTG TCGCTGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA	240
CACTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC	300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC	360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCC	405

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCACTCAGG ACTGCTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAATC	60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG	120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG	180
CTCAAGACTG TCGCTGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA	240
CACTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC	300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC	360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG	420

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGTCTGGAG GTAACGGATC CGGTGGCAAT GGGAGCGCG GAAATGGAAC CCAGGACTGC	360

TCCCTCCAAC ACAGCCCCAT CTCCTCCGAC TTGCTGTCA AAATCCGTGA GCTGTCTGAC	420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAG	465

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTCAG CCCCCCCCCA GCTGTCTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCGA CTCCTCAACC	300
CTGTCAGGGC GTAACGGCAG TGGAGGTAAT GGCACCCAGG ACTGCTCTT CCAACACAGC	360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT	420
TACCCAGTCA CGTGGCCTC CAACCTGCAG	450

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTCAG CCCCCCCCCA GCTGTCTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCGA CTCCTCAACC	300
CTGTCAGGGC GCAACGGCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCGAC	360
TCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG	420
GCCTCCAACC TGCAG	435

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTACCAAA	60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC	120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC	180

TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	AGGTAAACGGA	240
TCCGGTGGCA	ATGGGAGCGG	CGGAAATGGA	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCAGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTGCG	CTGGG		465

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATAACACTT	TGTACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	AGGTAAACGGA	240
TCCGGAGGTA	ATGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	300
GCTGTAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAAG	ATTACCCAGT	CACCGTGGCC	360
TCCAACCTGC	AGGACGAGGA	GCTCTGCGGG	GGCCTCTGGC	GGCTGGTCCCT	GGCACAGCGC	420
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG				450

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATAACACTT	TGTACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	CGGCAACGGC	240
ACGCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	300
GAGCTGTCTG	ACTACTGTCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	360
GAGGAGCTCT	GCGGGGGCCT	CTGGCAGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	420
AAGACTGTGCG	CTGGG					435

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCCTGGAG	GTAACGGCAG	TGGTGGCAAT	180
GGGAGCGGTG	GAAATGGAAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCAGGCTGGT	CCTGGCACAG	360
CGCTGGATGG	AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	420
GTGAACACGG	AGATACACTT	TGTACCAAAA	TGTGCCTTTC	AGCCC		465

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCAGGCG	GTAACGGCAG	TGGAGGTAAT	180
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCACATCCT	CCGACTTCGC	TGTCAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTCGGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	360
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	420
CACTTGTCA	CCAAATGTGC	CTTTCAGCCC				450

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCCTGGCG	GCAACGGCAG	GCAGGGACTGC	180
TCCCTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	240
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	300
GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	AGCAGGCTAA	GACTGTCGCT	360
GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTACCAAAA	420
TGTGCCTTTC	AGCCC					435

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTCAG	CCCCCCCCCA	GCTGTCTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAGTGGATC	CGGAGGTTCT	GGCAACCCAG	GACTGCTCCT	TCCAACACAG	360
CCCCATCTCC	TCCGACTTCG	CTGTAAAAT	CCGTGAGCTG	TCTGACTACC	TGCTTCAAGA	420
TTACCCAGTC	ACCGTGGCCT	CCAACCTGCA	G			451

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTCAG	CCCCCCCCCA	GCTGTCTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAGTGGATC	CGGTGGCAGT	GGGAGCGGCG	GATCTGGAAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGATCC					437

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GGATCCGGAG	GTACCCAGGA	CTGCTCCTTC	CAACACAGCC	CCATCTCCTC	CGACTTCGCT	60
GTCAAAATCC	GTGAGCTGTC	TGACTACCTG	CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	120
AACCTGCAGG	ACGAGGAGCT	CTGCGGGGGC	CTCTGGCGGC	TGGTCCTGGC	ACAGCGCTGG	180
ATGGAGCGGC	TCAAGACTGT	CGCTGGGTCC	AAGATGCAAG	GCTTGCTGGA	GCGCGTGAAC	240
ACGGAGATAC	ACTTGTAC	CAAATGTGCC	TTTCAGCCCC	CCCCCAGCTG	TCTTCGCTTC	300
GTCCAGACCA	ACATCTCCCG	CCTCCTGCAG	GAGACCTCCG	AGCAGCTGGT	GGCGCTGAAG	360
CCCTGGATCA	CTCGCCAGAA	CTTCTCCCGG	TGCCTGGAGC	TGCAGTGTCA	GCCCCACTCC	420
TCAACCCTGT	AAGCTT					436

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CCATGGCCAC	CCAGGACTGTC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGCTGTAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCAGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGCGG	TGGGTAGGA	GGTGGATCC				449

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCGGAG	GTGGCACCCA	GGACTGCTCC	TTCCAAACACA	GCCCCATCTC	CTCCGACTTC	60
GCTGTCAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAAG	ATTACCCAGT	CACCGTGGCC	120
TCCAACCTGC	AGGACGAGGA	GCTCTGCAGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	180
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG	TCCAAGATGC	AAGGCTTGCT	GGAGCGCGTG	240
AACACGGAGA	TACACTTTGT	CACCAAATGT	GCCTTTCAGC	CCCCCCCCAG	CTGTCTTCGC	300
TTCGTCCAGA	CCAACATCTC	CCGCCTCCTG	CAGGAGACCT	CCGAGCAGCT	GGTGGCGCTG	360
AAGCCCTGGA	TCACTCGCCA	GAACCTCTCC	CGGTGCCTGG	AGCTGCAGTG	TCAGCCCGAC	420
TCCTCAACCC	TGTAAGCTT					439

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CCATGGCCAC	CCAGGACTGTC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCAGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGGTCAGGA	GGTGGGTCAAG	GAGGTGGATC	C		461

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGATCCGGAG	GTGGCTCAGG	GGGAGGTTAGT	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	60
CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	120
TACCCAGTC	CCGTGGCCTC	CAACCTGCAG	GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	180
CTGGTCTGG	CACAGCGCTG	GATGGAGCGG	CTCAAGACTG	TCGCTGGTC	CAAGATGCAA	240
GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	CACTTGTCA	CCAAATGTGC	CTTTCAGCCC	300
CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	AACATCTCCC	GCCTCTGCA	GGAGACCTCC	360
GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	ACTGCCAGA	ACTTCTCCCG	GTGCCTGGAG	420
CTGCAGTGTC	AGCCCGACTC	CTCAACCCTG	TAAGCTT			457

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGCGGTG	GATCCGGAGG	TACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	360
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAAGATTA	CCCAGTCACC	420
GTGGCCTCCA	ACCTGCAG					438

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTC	TCACCAAATG	TGCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GATCCGGAGG	TGGCACCCAG	GACTGCTCCT	TCCAACACAG	CCCCATCTCC	360
TCCGACTTCG	CTGTCAAAAT	CCGTGAGCTG	TCTGACTACC	TGCTTCAAGA	TTACCCAGTC	420
ACCGTGGCCT	CCAACCTGCA	G				441

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTC	TCACCAAATG	TGCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGATCCCGA	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	360
CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	420
TACCCAGTCA	CCGTGGCCTC	CAACCTGCGAG				450

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTC	TCACCAAATG	TGCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300

CTGGGCGGTG GATCCGGAGG TGGCTCAGGG GGAGGTAGTG GTACCCAGGA CTGCTCCTTC	360
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAATCC GTGAGCTGTC TGACTACCTG	420
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAG	459

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTCAG CCCCCCCCCA GCTGTCTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGGGCGGTG GGTCAGGAGG TGGGTCAAGGA GGTGGATCCG GAGGTGGCAC CCAGGACTGC	360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTGCGTGTCA AAATCCGTGA GCTGTCTGAC	420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAG	465

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTCAG CCCCCCCCCA GCTGCCTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGGGCGGTG GGTCAGGAGG TGGGTCAAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT	360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA	420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG	480
CAG	483

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCCGATTACC CAGTCACCGT GGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC	60
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TGGCGGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGCTCA	AGACTGTCGC	TGGGTCCAAG	120
ATGCAAGGCT	TGCTGGAGCG	CGTGAACACG	GAGATACACT	TTGTCACCAA	ATGTGCCTT	180
CAGCCCCCCC	CCAGCTGTCT	TCGCTTCGTC	CAGACCAACA	TCTCCCGCCT	CCTGCAGGAG	240
ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	TGGATCACTC	GCCAGAACTT	CTCCCAGGTGC	300
CTGGAGCTGC	AGTGTCAAGCC	CGACTCCTCA	ACCCTGGCG	GTGGGTCAAGG	AGGTGGGTCA	360
GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATTCCTCC	420
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAA		465

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCGCCTCCA	ACCTGCAGGA	CGAGGGAGCTC	TGCGGGGCC	TCTGGCGGCT	GGTCCTGGCA	60
CAGCGCTGGA	TGGAGCGGCT	CAAGACTGTC	GCTGGGTCCA	AGATGCAAGG	CTTGCTGGAG	120
CGCGTGAACA	CGGAGATAAC	CTTGTCAACC	AAATGTGCCT	TTCAGCCCCC	CCCCAGCTGT	180
CTTCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	240
GGCGTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCTGGAGCT	GCAGTGTCA	300
CCCGACTCCT	CAACCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	360
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	420
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTG		465

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCCGTCGCTG	GGTCCAAGAT	GCAAGGCTTG	CTGGAGCGCG	TGAACACGGGA	GATAACACTT	60
GTCACCAAAT	GTGCCCTTCA	GCCCCCCCCC	AGCTGTCTTC	GCTTCGTCCA	GACCAACATC	120
TCCCGCCTCC	TGCAGGAGAC	CTCCGAGCAG	CTGGTGGCGC	TGAAGCCCTG	GATCACTCGC	180
CAGAACATTCT	CCCGGTGCCT	GGAGCTGCAG	TGTCAAGCCCG	ACTCCTCAAC	CCTGGGCGGT	240
GGGTCAGGAG	GTGGGTCAAGG	AGGTGGATCC	GGAGGTGGCA	CCCAGGACTG	CTCCTTCAA	300
CACAGCCCCA	TCTCCTCCGA	CTTCGCTGTC	AAAATCCGTG	AGCTGTCTGA	CTACCTGCTT	360
CAAGATTACC	CAGTCACCGT	GGCCTCCAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	420
TGGCGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGCTCA	AGACT		465

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATAACACTT	TGTACCAAA	60
TGTGCCTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCAGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGGCGG	TGGGTCAGGA	240
GGTGGGTCAG	GAGGTGGATC	CGGAGGTGGC	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTG	CTGGG		465

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GCCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACCTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	CTGGGCAGGTG	GGTCAGGAGG	TGGGTCAGGA	180
GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	360
CGCTGGATGG	AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	420
GTGAACACGG	AGATAACACTT	TGTACCAAA	TGTGCCTTC	AGCCC		465

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCCCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCGA	GCAGCTGGTG	60
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCTGGAGCT	GCAGTGTCA	120
CCCGACTCCT	CAACCCCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	180
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCCTGG	CACAGCGCTG	GATGGAGCGG	360
CTCAAGACTG	TCGCTGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	420
CACTTGTCA	CCAAATGTGC	CTTCAGCCC	CCCCCCAGCT	GTCTT		465

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCCACCAACA	TCTCCCGCCT	CCTGCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	60
TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	CTGGAGCTGC	AGTGTCAAGCC	CGACTCCTCA	120
ACCCCTGGCG	GTGGGTCAGG	AGGTGGGTCA	GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	180
TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	GAECTCGCTG	TCAAATCCG	TGAGCTGTCT	240
GACTACCTGC	TTCAAGATTA	CCCAGTCACC	GTGGCCTCCA	ACCTGCAGGA	CGAGGAGCTC	300
TGCGGGGGGCC	TCTGGCGGCT	GGTCCTGGCA	CAGCGCTGGA	TGGAGCGGCT	CAAGACTGTC	360
GCTGGGTCCA	AGATGCAAGG	CTTGCTGGAG	CGCGTGAACA	CGGAGATACA	CTTGTCAACC	420
AAATGTGCCT	TTCAAGCCCCC	CCCCAGCTGT	CTTCGCTTCG	TCCAG		465

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	
1					5				10					15		
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	
								20		25				30		
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	
								35		40				45		
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	
								50		55				60		
Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	
								65		70				75		80
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	
								85		90				95		
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	
								100		105				110		
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	
								115		120				125		
Glu	Leu	Gln	Cys	Gln	Pro											
					130											

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala
 1 5 10 15
 Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30
 Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp
 35 40 45
 Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala
 50 55 60
 Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
 65 70 75 80
 Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe
 85 90 95
 Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
 100 105 110
 Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
 115 120 125
 Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
 130 135

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala
 1 5 10 15
 Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30
 Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp
 35 40 45
 Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala
 50 55 60
 Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His
 65 70 75 80
 Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe
 85 90 95
 Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu
 100 105 110
 Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu
 115 120 125
 Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser
 130 135 140
 Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu
 145 150 155 160
 Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Ala Ala Ala
 165 170 175
 Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly
 180 185 190
 Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu
 195 200 205

His

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACCCAGGACT	GCTCCTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTACCCA	AATGTGCCTT	TCAGCCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCGAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTCAAGC	CCAGACCAAC		402

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACCCAGGACT	GCTCCTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTACCCA	AATGTGCCTT	TCAGCCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCGAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTCAAGC	CCGACTCCTC	AACCCCTGCCA	420
CCCCCATGGA	GTCCCCGGCC	CCTGGAGGCC	ACAGCCCCGA	CAGCCCCCGCA	GCCCCCTCTG	480
CTCCTCTTAC	TGCTGCTGCC	CGTGGGCCTC	CTGCTGCTGG	CCGCTGCCCTG	GTGCCCTGCAC	540
TGGCAGAGGA	CGCGGCGGAG	GACACCCCGC	CCTGGGGAGC	AGGTGCCCTCC	CGTCCCCAGT	600
CCCCAGGACC	TGCTGCTTGT	GGAGCACTGA				630

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser

1 5 10 15
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly
20 25

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr Ala
1 5 10 15
Gly Gln Pro Pro Leu
20

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Val Glu Thr Val Phe His Arg Val Ser Gln Asp Gly Leu Leu Thr Ser
1 5 10 15